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BMS 353
Bioinformatics for Biomedical Science

Module coordinator: Dr Marta Milo
Research Software Instructor: Dr Mike Croucher

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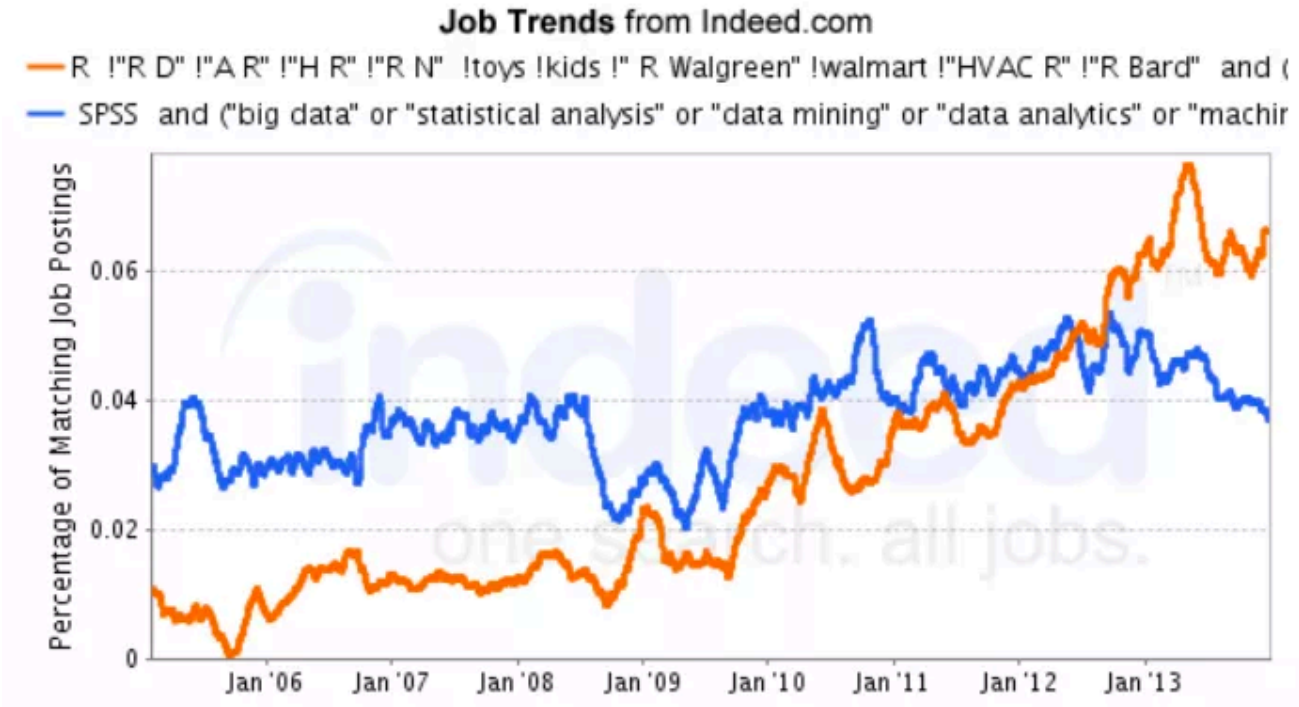
An Introduction to the tools we'll be using

R is a free language and environment for statistical computing and graphics.



How popular is R? http://r4stats.com/articles/popularity/

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An Introduction to the tools we'll be using

Packages
Save time by using other people's code.

Comprehensive R Archive Network (CRAN)
7468 packages (November 2015)
https://cran.r-project.org/web/packages/

Bioconductor
OPEN SOURCE SOFTWARE FOR BIOINFORMATICS

Bioconductor
1104 packages (November 2015)
https://www.bioconductor.org/

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Open source, interactive data science and scientific computing across over 40 programming languages.

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jupyter

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Currently in use at

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Combine live computer code, data, text and mathematics in one interactive document.

Academic papers only give a description of your analysis.

Jupyter notebooks contain both the description and the analysis itself.

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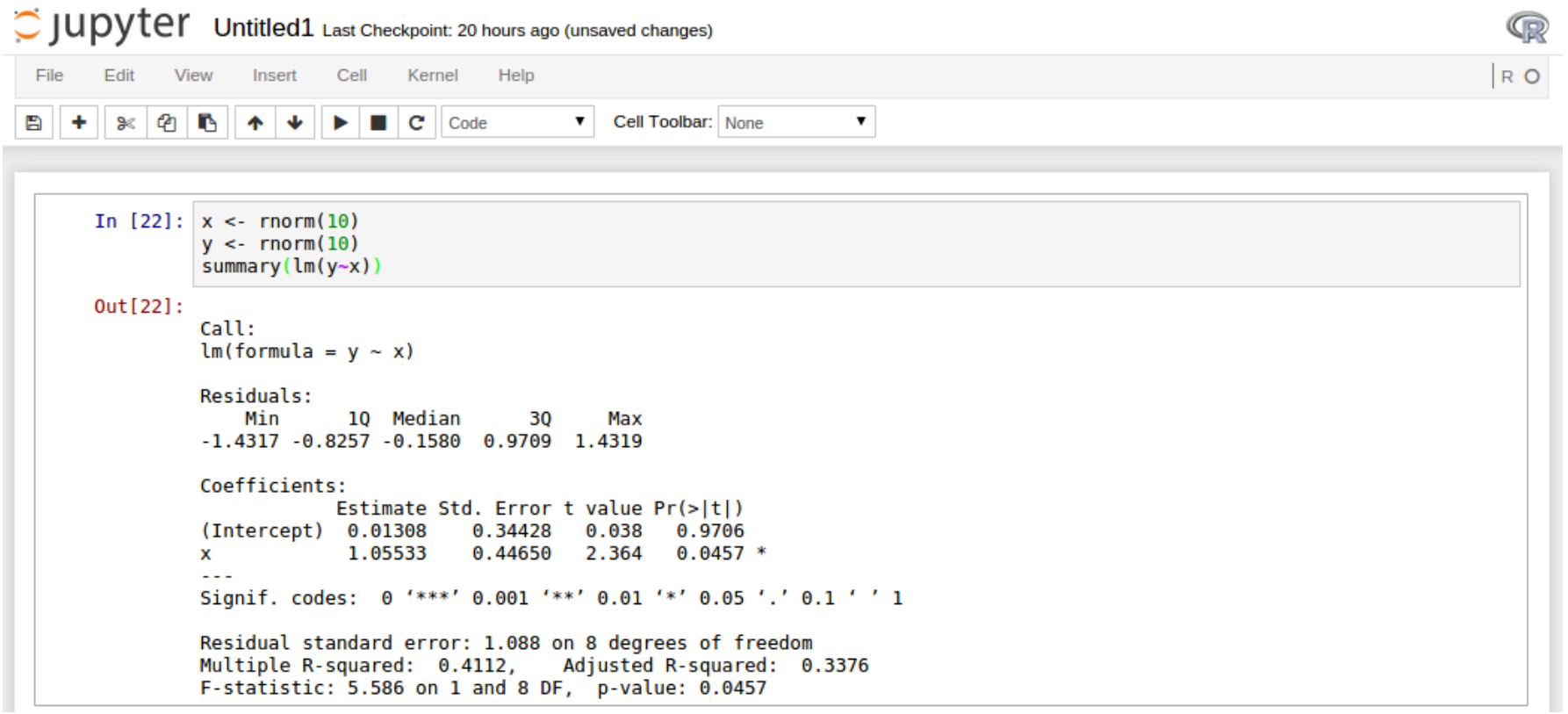

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Collaborative computational mathematics

An open source environment for running Jupyter notebooks (and others!) in the cloud.

Dedicated Virtual Machine for this course on the Google Cloud Platform.

As powerful as a node on the Sheffield University Supercomputer: Iceberg

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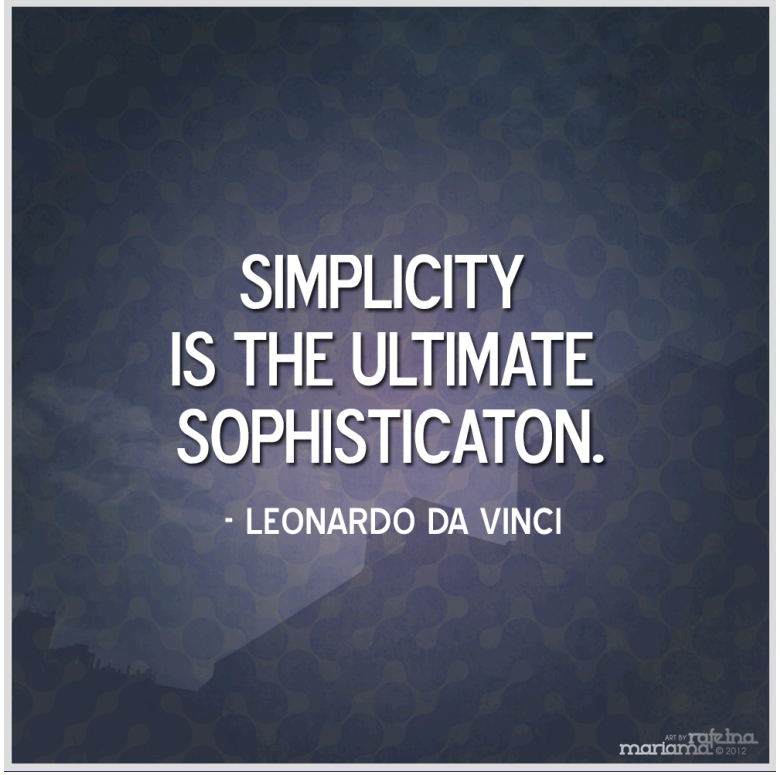

All you need is a web browser and internet connection.

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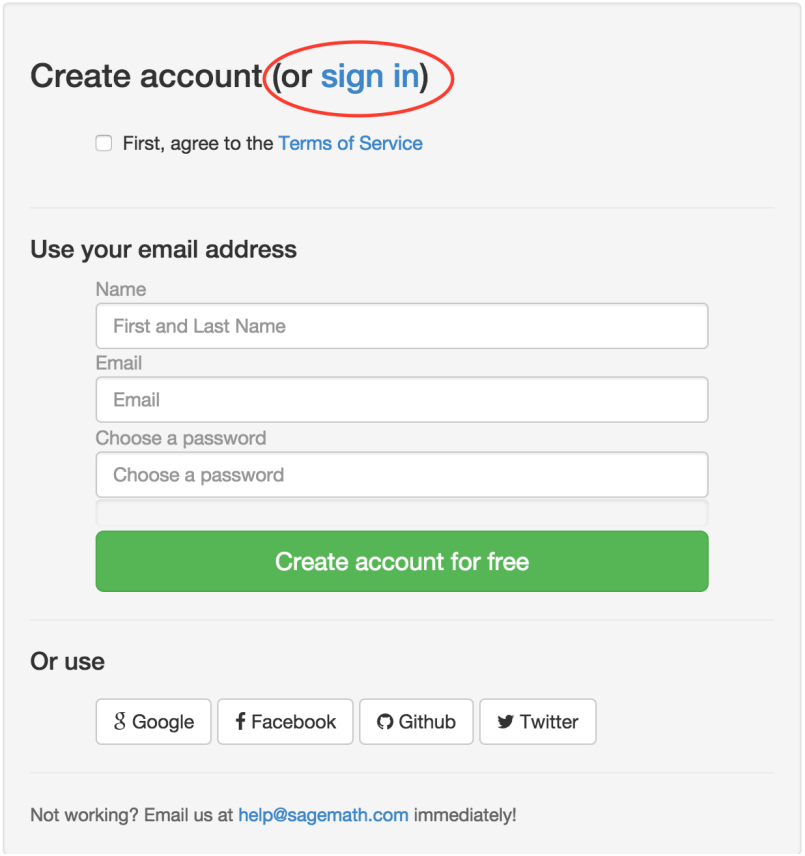
Log into SageMathCloud
https://cloud.sagemath.com/

Your username and password have been created for you.



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